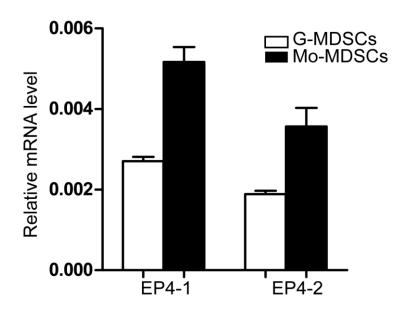
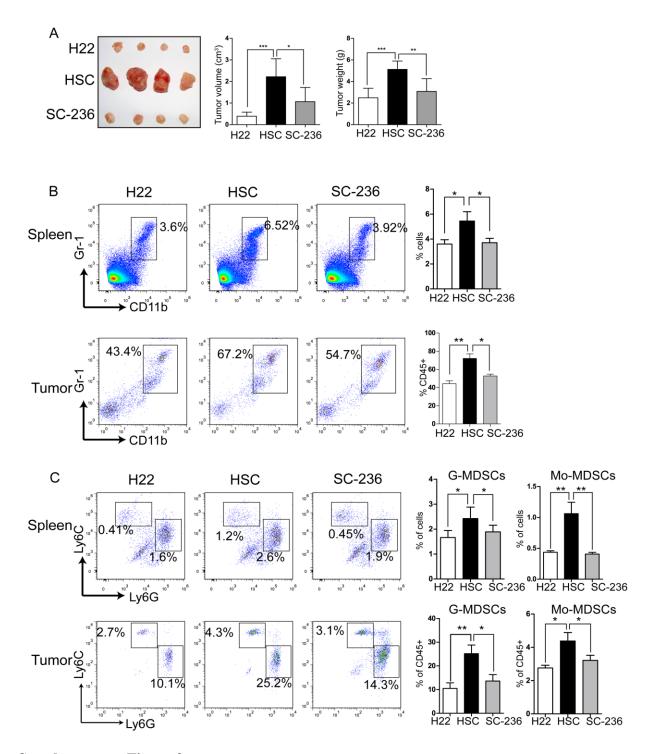
# Activated hepatic stellate cells promote liver cancer by induction of myeloid-derived suppressor cells through cyclooxygenase-2

## **Supplementary Material**



### **Supplementary Figure 1**

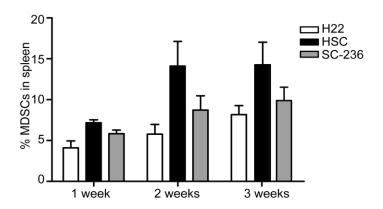
EP4-1 and EP4-2 expression. G-MDSCs and Mo-MDSCs were sorted with MACS and EP4-1 and EP4-2 mRNA was measured with RT-PCR. Data are expressed as means  $\pm$  SD relative to GAPDH.



## **Supplementary Figure 2**

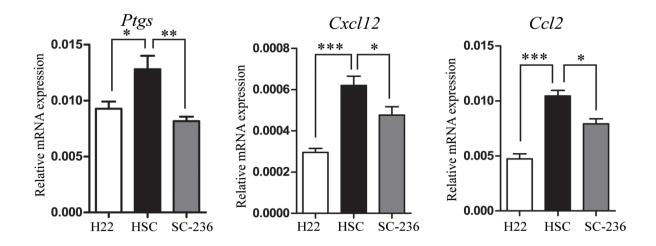
HSCs promoted growth of HCC by induction of MDSCs via PGE<sub>2</sub> signaling. (A) Representative tumor samples, tumor volume and weight. (B) MDSCs in splenocytes and tumors were detected by flow cytometry; number is percent of the cell population represented by MDSCs (right

panels). Percent MDSCs was calculated using the formula: corrected MDSC percent =  $100\% \times \text{CD11b}^+\text{ Gr-1}^{+/\text{low}}$  percent  $\times \text{CD45}^+\text{ percent}$ . (C) G-MDSCs and Mo-MDSCs were measured with flow cytometry. Number is percent of the cell population represented by G-MDSCs and Mo-MDSCs (right panels) and these were calculated as follows: corrected G-MDSC percent =  $100\% \times \text{CD11b}^+\text{ percent} \times \text{Ly6G}^+\text{Ly6C}^{\text{low}}$  percent  $\times \text{CD45}^+\text{ percent}$ . Corrected Mo-MDSC percent =  $100\% \times \text{CD11b}^+\text{ percent} \times \text{Ly6G}^-\text{Ly6C}^{\text{high}}$  percent  $\times \text{CD45}^+\text{ percent}$ . Data represent 3 independent experiments and are expressed as means  $\pm \text{SD}$ ; \*P < 0.05, \*\*P < 0.01, \*\*\*P < 0.001.



### **Supplementary Figure 3**

Splenic MDSC populations in mice at 1, 2, and 3 weeks after tumor injection. Percent of MDSCs in spleen of tumor-bearing mice at indicated time. A subcutaneous mouse model was used to exclude increased MDSCs in the HSC group due to greater tumor burdens.



# **Supplementary Figure 4**

Expression of cytokines and chemokines in the tumor microenvironment. The mRNA expression of *Ptgs2*, *Cxcl12*, and *Ccl2* in the tumor microenvironment was detected using RT-PCR.